



SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Levy, Gary  
Clark, David A.
- (ii) TITLE OF INVENTION: Methods of Modulating Immune Coagulation
- (iii) NUMBER OF SEQUENCES: 4
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: BERESKIN & PARR  
(B) STREET: 40 King Street West  
(C) CITY: Toronto  
(D) STATE: Ontario  
(E) COUNTRY: Canada  
(F) ZIP: M5H 3Y3
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Floppy disk  
(B) COMPUTER: IBM PC compatible  
(C) OPERATING SYSTEM: PC-DOS/MS-DOS  
(D) SOFTWARE: PatentIn Release #1.0, Version #1.30
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: 09/442,143  
(B) FILING DATE: 15-NOV-1999  
(C) CLASSIFICATION:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Gravelle, Micheline  
(B) REGISTRATION NUMBER: 40,261  
(C) REFERENCE/DOCKET NUMBER: 9579-014
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: (416) 364-7811  
(B) TELEFAX: (416) 361-1398

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 4630 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: other nucleic acid
- (vi) ORIGINAL SOURCE:  
(A) ORGANISM: Homo sapiens
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GATCTAGGGT TGGAAGCCAG GTCTCCTGAG TATGCGAGAA TAAATACAGT CATGGAAGTG	60
TAAAGAGTCT GCCAACATTT TGAGAAATGTG AATAGGATTT GGCTAAAATT AAGGGGATAT	120
ACAGAAAAGT CATAGGAAAT CAGGTTAAAG ACATAAATAT GAGATAGGCT ACAGAGTGTT	180
TTAAGTAATA CAATAAAACA TTTAGATTTT TGCCCATGTC AGTCATTTTG AAATTATTTT	240
TAAAGCAAAA AAACCCTTTT TAAACAAGAA ATCTTATGAG ATGTCAATAT GCAAAACAAA	300
TTAAAAGGAG GTGGTTTCTC TAACTGAAGC TGTTCTCTT TCCTGCCTTC AGCCTCTGAA	360

GAGAAAGTTA GAAAACTATT ATCATTAAATG CTACATGTTT TGAACAAGCT GATATACCAA 420  
GTGGCCCAGA GAGCAGGTAG AAGAACCAGC GTGGAGACAG AAAGCAAGAG GCCCGCCTGC 480  
CAGGGCTACC TGCAGAAAGA AAGGGCAAAG ATGCTGTAGG CAAGAGAAAGT TCAGGACAGA 540  
CACTGGCATA GCTCAAAGAT TCACATTGGA GCAGCTGTGG AAGATGACAG TACAATTACC 600  
AAAATGTCGA AGGGCAAAGG AGGCAGCTAC TGGTTTTGAT GAAAGACAAT TATGTCCTTT 660  
TAAATGGGTC TTAGACATTT AGACATTTAT ATACACTATG CTACGGACAA AGGAATAGAA 720  
AGTAGCACTT TTTTCTCCAC TAGTTTTCTT CTCTTTTTCA AGTAGATGAA GCAAAAGTCA 780  
ACTGCAATAG TCAGAAAGCT GTACTTTGTT ACACTTAGAA ACTTCTAAAA GTGCTTAAGA 840  
TTTCACCTGA AAGTCCAACA TGAAGAAAAT ACAGGCTCCC CAATGCCCCA TTCTAAGAAG 900  
GAAAAAGGAC CATTTTCATT TTAGTAACGT TTCTGTTCTA TAGACAGTTT GGATAACTAG 960  
CTCTTACTTT TTATCTTTAA AAACGTGTTT TCCAGTGAAG TTACGTATAA TTATTTACTT 1020  
CAAGCGTAGT ATACCAAATT ACTTTAGAAA TGCAAGACTT TTCTTATACT TCATAAAATA 1080  
CATTATGAAA GTGAATCTTG TTGGCTGTGT ACATTTGACT ATAATAATTT CAATGCATAT 1140  
TATTTCTATT GAGAGTAAGT TACAGTTTTT GBCAACTGC GTTTGATGAG GGCTATCTCC 1200  
TCTTCCTGTG CGTTTCTAAA ACTTGTGATG CAAACGCTCC CACCCTTTCC TGGGAACACA 1260  
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TGGGGTGAGC AGCACTGTAA AGATGAAGCT GGCTAACTGG TACTGGCTGA GCTCAGCTGT 1380  
TCTTGCCACT TACGGTTTTT TGGTTGTGGC AAACAATGAA ACAGAGGAAA TTAAAGATGA 1440  
AAGAGCAAAG GATGTCTGCC CAGTGAGACT AGAAGCAGA GGGAAATGCG AAGAGGCAGG 1500  
GGAGTGCCCC TACCAGGTAA GCCTGCCCCC CTTGACTATT CAGCTCCCGA AGCAATTCAG 1560  
CAGGATCGAG GAGGTGTTCA AAGAAGTCCA AAACCTCAAG GAAATCGTAA ATAGTCTAAA 1620  
GAAATCTTGC CAAGACTGCA AGCTGCAGGC TGATGACAAC GGAGACCCAG GCAGAAACGG 1680  
ACTGTTGTTA CCCAGTACAG GAGCCCCGGG AGAGCTTGGT GATAACAGAG TTAGAGAATT 1740  
AGAGAGTGAG GTTAACAAGC TGTCTCTGA GCTAAAGAAT GCCAAAGAGG AGATCAATGT 1800  
ACTTCATGGT CGCCTGGAGA AGCTGAATCT TGTAATATG AACAACATAG AAAATTATGT 1860  
TGACAGCAAA GTGGCAAATC TAACATTTGT TGTCAATAGT TTGGATGGCA AATGTTCAAA 1920  
GTGTCCCAGC CAAGAACAAA TACAGTCACG TCCAGGTATG TATAATAATG TTTTCTTATC 1980  
ATATGTTTAT AAATGTTATA CAGTCAGAGA TGTATCTAAA AGATTAACCT GAGTCAGTAA 2040  
GTTAAATAGA TGACAGATTA AGTCTTTTAT TTATCAAGGT GCACAGGAAA AAATAAATAT 2100  
CTTCTCAAAT ATGACCACAT AAATATGACC TAATTACAAA ATCATAGTTA GTTCTGTATC 2160  
CACTGGAAGT CACTTTCAAT TTTAAGATCT TATTTGTTAA TGCCAGACCT ACTTGCAAGC 2220  
AGAGATTAGA GGTCTTTTCT GCTTTATAAC ATTAGTTCT TCTTGTGAGG CCTTAAGCAT 2280  
TTACTAAACA CCTTCAAGTA AGTTTAGTAA AGTTTCATTA CTGCCATTGA TTCAATTATC 2340

AAACTGCTTT TGTACATATA AAGAATTCTT CAGATGCATG GTTCTATTA ACAAGATCCA 2400  
ATGCCTTCCT TTTATTTCCC CTTCAGTTCA ACATCTAATA TATAAAGATT GCTCTGACTA 2460  
CTACGCAATA GGCAAAAGAA GCAGTGAGAC CTACAGAGTT ACACCTGATC CCAAAAATAG 2520  
TAGCTTTGAA GTTTACTGTG ACATGGAGAC CATGGGGGA GGCTGGACAG TGCTGCAGGC 2580  
ACGTCTCGAT GGGAGCACCA ACTTCACCAG AACATGGCAA GACTACAAAG CAGGCTTTGG 2640  
AAACCTCAGA AGGGAATTTT GGCTGGGGAA CGATAAAATT CATCTTCTGA CCAAGAGTAA 2700  
GGAAATGATT CTGAGAATAG ATCTTGAAGA CTTTAATGGT GTCGAACTAT ATGCCTTGTA 2760  
TGATCAGTTT TATGTGGCTA ATGAGTTTCT CAAATATCGT TTACACGTTG GTAACATAA 2820  
TGGCACAGCT GGAGATGCAT TACGTTTCAA CAAACATTAC AACCACGATC TGAAGTTTTT 2880  
CACCCTCCA GATAAAGACA ATGATCGATA TCCTTCTGGG AACTGTGGGC TGTACTACAG 2940  
TTCAGGCTGG TGGTTTGATG CATGCTTTTC TCCAAACCTA AATGGCAAAT ATTATCACCA 3000  
AAAATACAGA GGTGTCCGTA ATGGGATTTT CTGGGTACC TGGCCTGGTG TAAGTGAGGC 3060  
ACACCTGGT GGCTACAAGT CCTCCTTCAA AGAGGCTAAG ATGATGATCA GACCCAAGCA 3120  
CTTTAAGCCA TAAATCACTC TGTTCACTCC TCCAGGTATT CGTTATCTAA TAGGGCAATT 3180  
AATTCCTTGT TTCATATTTT TCATAGCTAA AAAATGATGT CTGACGGCTA GGTTCTTATG 3240  
CTACACAGCA TTTGAAATAA AGCTGAAAAA CAATGCATTT TAAAGGAGTC CTTTGTGTGT 3300  
ATGCTGTTAT CCAATGAACA CTTGCAAGCA ATTAGCAATA TTGAGAATTA TACATTAGAT 3360  
TTACAATTCT TTTAATTTCT ATTGAACTT TTTCTATTGC TTGTATTACT TGCTGTATTT 3420  
AAAAATAAT TGTTGGCTGG GTGTGGTAGC TCACGCCTGT AATCCCAGCA CTTTGGAAATG 3480  
TCAAGGCAGG CAGATCACTT GAGGTCAGGA GTTTGAGACC AGCCTGGCCA AACATGTGAA 3540  
ACGCTGTCTC TATTAATAAT AAAAAATTA GCCGGGCATG GTGGTACATG CCTGTAATCA 3600  
ACGCTGTTTA TTAAAAATAC AAAAATTAGC CGGGCATGGT GGACATGCCT GTAATCCTAG 3660  
TACTTGGGAG GCTGAGGCAG GAGAATCGCT TGAACCTGAG AGGAAGAGGT TGCAGTGAGC 3720  
CAAGAATGAG CCACTGCACT CCAGCATGGG TGACAGAGAA AACTCTGTCT CAAACAAAAA 3780  
AATAATAAAA TTTATTCAGT AGGTGGATTC TACACAAAGT AATCTGTATT TGGGCCATGA 3840  
TTTAAGCACA TCTGAAGGTA TATCACTCTT TTCAGGCTAT AATTATTTGG GTAATCTTCA 3900  
TTCTGAGACA AACTTAATCT ATATCATTTA CTTTGCAACA GAACAACCTT ACAGCATTTT 3960  
GGTCCCAGA CTAAGGGAAC TAATATCTAT ATAATTAAAC TTGTTCAATT ATCATTCATG 4020  
AAATATAAAA TACTTGTCAT TTAAACCGTT TAAAAATGTG GTAGCATAAT GTCACCCCAA 4080  
AAAGCATTC AAGGCAATG TAACTGTGAA GACCAGGTT TAAAGGTAAT TCATTTATAG 4140  
TTTATAACTC CTTAGATGTT TGATGTTGAA AACTGCTTTA ACATGAAAT TATCTTCCTC 4200  
TGCTCTGTGT GAACAATAGC TTTTAATTTA AGATTGCTCA CTACTGTACT AGACTACTGG 4260  
TAGGTTTTTT TGGGGGGGGG TGGGTAGGGA TATGTGGGTA ATGAAGCATT TACTTACAGG 4320

CTATCATACT CTGAGGCCAA TTTTATCTCC AAAGCAATAA TATCATTAAG TGATTCACTT 4380  
 CATAGAAGGC TAAGTTTCTC TAGGACAGAT AGAAAACATG AATTTTGAAA TATATAGAAC 4440  
 AGTAGTTAAA ATACTATATA TTTCAACCTT GGCTGGTAGA TTGCTTATTT TACTATCAGA 4500  
 AACTAAAAGA TAGATTTTAA CCCAAACAGA AGTATCTGTA ATTTTATATA TTCATCAATT 4560  
 CTGGAATGCT ATATATAATA TTTAAAAGAC TTTTAAATG TGTTTAATTT CATCATCGTA 4620  
 AAAAGGGATC 4630

(2) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:  
 (A) LENGTH: 439 amino acids  
 (B) TYPE: amino acid  
 (C) STRANDEDNESS: single  
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met Lys Leu Ala Asn Trp Tyr Trp Leu Ser Ser Ala Val Leu Ala Thr  
 1 5 10 15  
 Tyr Gly Phe Leu Val Val Ala Asn Asn Glu Thr Glu Glu Ile Lys Asp  
 20 25 30  
 Glu Arg Ala Lys Asp Val Cys Pro Val Arg Leu Glu Ser Arg Gly Lys  
 35 40 45  
 Cys Glu Glu Ala Gly Glu Cys Pro Tyr Gln Val Ser Leu Pro Pro Leu  
 50 55 60  
 Thr Ile Gln Leu Pro Lys Gln Phe Ser Arg Ile Glu Glu Val Phe Lys  
 65 70 75 80  
 Glu Val Gln Asn Leu Lys Glu Ile Val Asn Ser Leu Lys Lys Ser Cys  
 85 90 95  
 Gln Asp Cys Lys Leu Gln Ala Asp Asp Asn Gly Asp Pro Gly Arg Asn  
 100 105 110  
 Gly Leu Leu Leu Pro Ser Thr Gly Ala Pro Gly Glu Val Gly Asp Asn  
 115 120 125  
 Arg Val Arg Glu Leu Glu Ser Glu Val Asn Lys Leu Ser Ser Glu Leu  
 130 135 140  
 Lys Asn Ala Lys Glu Glu Ile Asn Val Leu His Gly Arg Leu Glu Lys  
 145 150 155 160  
 Leu Asn Leu Val Asn Met Asn Asn Ile Glu Asn Tyr Val Asp Ser Lys  
 165 170 175  
 Val Ala Asn Leu Thr Phe Val Val Asn Ser Leu Asp Gly Lys Cys Ser  
 180 185 190  
 Lys Cys Pro Ser Gln Glu Gln Ile Gln Ser Arg Pro Val Gln His Leu  
 195 200 205  
 Ile Tyr Lys Asp Cys Ser Asp Tyr Tyr Ala Ile Gly Lys Arg Ser Ser  
 210 215 220

Glu Thr Tyr Arg Val Thr Pro Asp Pro Lys Asn Ser Ser Phe Glu Val  
225 230 235 240

Tyr Cys Asp Met Glu Thr Met Gly Gly Gly Trp Thr Val Leu Gln Ala  
245 250 255

Arg Leu Asp Gly Ser Thr Asn Phe Thr Arg Thr Trp Gln Asp Tyr Lys  
260 265 270

Ala Gly Phe Gly Asn Leu Arg Arg Glu Phe Trp Leu Gly Asn Asp Lys  
275 280 285

Ile His Leu Leu Thr Lys Ser Lys Glu Met Ile Leu Arg Ile Asp Leu  
290 295 300

Glu Asp Phe Asn Gly Val Glu Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr  
305 310 315 320

Val Ala Asn Glu Phe Leu Lys Tyr Arg Leu His Val Gly Asn Tyr Asn  
325 330 335

Gly Thr Ala Gly Asp Ala Leu Arg Phe Asn Lys His Tyr Asn His Asp  
340 345 350

Leu Lys Phe Phe Thr Thr Pro Asp Lys Asp Asn Asp Arg Tyr Pro Ser  
355 360 365

Gly Asn Cys Gly Leu Tyr Tyr Ser Ser Gly Trp Trp Phe Asp Ala Cys  
370 375 380

Leu Ser Ala Asn Leu Asn Gly Lys Tyr Tyr His Gln Lys Tyr Arg Gly  
385 390 395 400

Val Arg Asn Gly Ile Phe Trp Gly Thr Trp Pro Gly Val Ser Glu Ala  
405 410 415

His Pro Gly Gly Tyr Lys Ser Ser Phe Lys Glu Ala Lys Met Met Ile  
420 425 430

Arg Pro Lys His Phe Lys Pro  
435

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 5403 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: other nucleic acid

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

CATAAGGCGT GTCTGACAAA TTCTTCATAC ACACATTTCC CCTTTGCACA TTCAGTCTGT	60
ATAGGTTATT TCTATAGGAG AAAAAAATA TTCAAATTCC TTGTGCACTG GTAACAGGCA	120
TGAAGGCTCA GCAAAGCCAA TACGTGTTAT GTCCAGTTGG AGACAGTGCC AGGGCCAACA	180
TTCCAGACTT CTCAGATAGA AAGTGCGCCT GCCTGCCCTG CTCTGAGAAT TTGAAGAGAG	240
TAGTTCAGTT AGAATTAAGA GGCAGTAGAG AAAAGTCTTG GGAAATCTGG TTAGAGATAT	300
AAATATGAGA ACTGGACATG GTGGTACACA CCTGTGATCT CTGTGTTTAG GAGGGAGAGG	360

h1

CAGAGAGATC	AGGAGTTCAA	GGCCAGCCTG	AGCTACTTGA	GACCCAGTCT	AAATAAATAA	420
GAGATAGATT	ACAGAGTGCC	TTTAACTAGT	ACAGAGAAAG	AATTTGGGTT	TATCTGTGTC	480
AGTTACGCTG	AAATAATTTT	TAAGTAATAA	AATCCCTTTT	AATAAGAAAC	CTTATGAGGT	540
CAGTATGCAC	AATGAACTTA	AGAGAGACCC	CCAGCTCCTG	AGCTGAGTGA	TGGGGAAGGA	600
CAGCCACTGC	CTGTGATGTG	TGAGTGACGT	GCTTCCAAGT	GTTTTAACCA	CTGACGATTA	660
CATAGCCTGC	ACAGTCAGGA	GAAAACAGCC	GTATTCTCTG	CCAGTTCTCT	TCCCTTTTAC	720
AAACAGATGA	GAGACACACA	CAGAGAATCC	ATTTAAAGAG	CGGACCTTTG	TTCTGATTAG	780
GGGCAATTTT	AAGTACTTAA	GAGTTCACAC	AAAGTCTAGC	CTTCAAAAAG	AAAACAGGTT	840
CCCAAACCTAG	GGAGGAAACA	GAATCATTTC	CATTTTGGTG	ACATTTAGTG	GGAAGAAGCT	900
CACAGACATT	TAGACGTTCC	AACTCTTTCC	CCACTAGTGG	ACCAAGTATA	TAATATGGTA	960
TCTTTTGGGC	ACTGGTATTA	CAACTGTTTT	TTAAACAAAA	GACTTTCCTT	GTGCTTTACT	1020
AAAAACCCAG	ACGGTGAATC	TTGAATACAA	TGCGTGCCAC	CCACGGCAGG	CATTCTATTG	1080
TGCATAGTTT	TGACTGACAG	GAGATGACAG	CATTTGGCTG	GCTGCGCTTG	CTGAGGACCC	1140
TCTCCTCCTG	TGTGGCGTCT	GAGACTGTGA	TGCAAATGCG	CCCGCCCTTT	TCTGGGAACT	1200
CAGAACGCCT	GAGTCAGGCG	GCGGTGGCTA	TTAAAGCGCC	TGGTCAGGCT	GGGCTGCCGC	1260
ACTGCAAGGA	TGAGGCTTCC	TGGTTGGTTG	TGGCTGAGTT	CTGCCGTCCT	CGCTGCCCTGC	1320
CGAGCGGTGG	AGGAGCACAA	CCTGACTGAG	GGGCTGGAGG	ATGCCAGCGC	CCAGGCTGCC	1380
TGCCCCGCGA	GGCTGGAGGG	CAGCGGGAGG	TGCGAGGGGA	GCCAGTGCCC	CTTCCAGCTC	1440
ACCCTGCCCC	CGCTGACCAT	CCAGCTCCCG	CGGCGCTTG	GCAGCATGGA	GGAGGTGCTC	1500
AAAGAAGTGC	GGACCCCTCA	GGAAGCAGTG	GACAGTCTGA	AGAAATCCTG	CCAGGACTGT	1560
AAGTTGCAGG	CTGACGACCA	TCGAGATCCC	GGGGGAATG	GAGGGAATGG	AGCAGAGACA	1620
GCCGAGGACA	GTAGAGTCCA	GGAAGTGGAG	AGTCAGGTGA	ACAAGCTGTC	CTCAGAGCTG	1680
AAGAATGCAA	AGGACCAGAT	CCAGGGGCTG	CAGGGGCGCC	TGGAGACGCT	CCATCTGGTA	1740
AATATGAACA	ACATTGAGAA	CTACGTGGAC	AACAAGTGG	CAAATCTAAC	CGTTGTGGTC	1800
AACAGTTTGG	ATGGCAAGTG	TTCCAAGTGT	CCCAGCCAAG	AACACATGCA	GTCACAGCCG	1860
GGTAGGTGTA	ATGAGGGTCA	TACAGTTTGT	TCATGAAAGC	TGTATAGCCA	GATAGTGGCC	1920
ATAAACATTA	ACCCGAGGGA	GCATAAGTTA	GTCAGACTTT	CACCTGTTAA	GTTATGGCAG	1980
GAGAAACAAG	TGTTTTCTCA	AATGAGACAA	CAGAAATGGT	AAATGATCCA	CGTACAAAAA	2040
TCCTATTAGT	TGTACTCGTT	AGAGACCGTC	ACTTGCAAGT	CTCTAGACCT	TCCCTGCTAG	2100
GTCGACCAAC	AGACGAGCAG	AAACAGATTG	CTCCCGCAAT	CTGAACACAT	ATTTGAACAC	2160
AGGACAGGTA	TGGCAAGGTT	CCTGGCTCTG	CTTGCTTAGG	TCCCTGGGAA	TCAGATCTTG	2220
GGTGGCTGAT	GGGCTTTATA	AGGCTTTCAC	AAACAATCTG	CTGTGCTAGG	TTCTCAAATA	2280
TCTAGTGAGA	ATGGGAGATT	TTTATACATG	GAAGCATCTC	TCCTCTCTCT	CTCCTCTCTC	2340

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CTCCCTCCCT CCCTCTCTCT CTCTTTGTGT GCGTGTGTGG TGGGGATGAG GACACGTGTA 2460  
GAACTTCGGG GGTGAGACT TAGTGCAAT GCATCCTCAC CATTCCAGTT AGTGAATGTT 2520  
AACACTATTT AAGGTCACAG ACCTAACAGC CTTCTGTGTC CGGATTCCTG GATTCCTAGG 2580  
ACCTTTGTGG ATGGGTGACC ACACCCCTCTG TGTTCATCCT GACTGTGAGG TCGATGGGAC 2640  
ATAGTAGGGA TAACTTTCAT TTGGAATCTC TAGAGATGGT AGGTCATCAT GTCATAGAAT 2700  
GTTATCACTA ATGACCAAGA TAGACACTCA TGTTTAAGAG ACATCACAAG GTGTATATTA 2760  
AATATGACAT GGCATATAAC TTGTAATGAC AAAAAATAT TCTGTTACCT ACTTTTCTCC 2820  
TAAAAGCTTG GGACTCTCCA GAGTTCTAAA TACATGCAA CAGATTATTG TGTTTTACAG 2880  
GAATCTTATA TTGAACTTTC TTTACCTGAC TCAAATTTTA TTAAAATTAA CTGGGAACAA 2940  
ATAGTTGGTC TCTAATCTCT AAAAAACCA CCAAATGATT AACTGAGCA TAATTATAAT 3000  
CACCTGCTG CTACGTCTAG AAACCAAACCT GTGAAATATT GGCTGACTGT ATACCTTCCT 3060  
AAATAATAAA TTCAGGATAA CATTGCCATA TTATTGGAGA ACCCCCCCT CCCTTTTAAA 3120  
ACTGGAATCA TTTTATGTCA ATCTCAGGTG AAATACGAAT GGGTTTCAGA ACAGTGCTGT 3180  
GCACTGAAGG CTGACATTTA GAACATATAT AACGATTTCT GTAAAGTCTG CTGTAACAAT 3240  
TGCTGATTGT ATCCTAGGAG ACTTGACTC CTCTCAACGT TAAGGCAGAG GAATATAATG 3300  
GTTATGAGAG TAAAACTCTC TGTCAGGTAC ATCTGGCTTT CTGTCCCAGC TCTGTCACTT 3360  
AACACTTAGT TCGGGTGGGA AAAC'TCCCTG ATCTTCCGGG AGACTAAGTA ACTGTATAAG 3420  
CAAGCTGGCC GTGATATCCA CGTCGTAAG CTGCTGTGTG GGTTCAGTGA AAAGTGTAC 3480  
AGTGATTGGC AGAGTTTCTG GAGGTCATTG ACCCTCATTA AACCTTGCAT AACTTATTC 3540  
TTACTACTCT TTGCTGTTAG TGTTGCCACC AGGATTGCCA TTCAAGGCAG TCCTGTATAC 3600  
TTGATAACAC CAGTTGGTTC TGAGGCCTTA GTTAGCATCT GTTAGCCTGG TTCAGGAGAG 3660  
TGTATCAGAG CCAGGTTCCCT CTATCACATA AACTGTAACG CAAGTGAATT GTCCAATTGC 3720  
TGTTGAGTCT GAGAGTCCTT GAGGTGCATA GCTTTGACTA ATAAATCCCC ATGCTTTTAT 3780  
GCTTTTCCTT CCTCCCTCTT CCAGTTCAAC ATCTAATATA CAAAGATTGT TCCGACCACT 3840  
ACGTGCTAGG AAGGAGAAGC AGTGGGGCCT ACAGAGTTAC CCCTGATCAC AGAAACAGCA 3900  
GCTTTGAGGT CTAAGTGAC ATGGAGACCA TGGGTGGAGG CTGGACGGTG CTGCAGGCTC 3960  
GCCTTGATGG CAGCACCAC TTCAACAGAG AGTGGAAAGA CTACAAAGCC GGCTTTGGAA 4020  
ACCTTGAACG AGAATTTTGG TTGGGCAACG ATAAATTTCA TCTTCTGACC AAGAGTAAGG 4080  
AAATGATTTT GAGAATAGAT CTTGAAGACT TTAATGGTCT CACACTTTAT GCCTTGATG 4140  
ATCAGTTTTA TGTGGCTAAT GAATTTCTCA AATACCGATT ACACATCGGT AACTACAATG 4200  
GCACGGCAGG GGATGCCTTG CGTTTCAGTC GAACTACAA CCATGACCTG AGGTTTTTCA 4260  
CAACCCCAAG CAGAGACAAC GATCGGTACC CCTCTGGGAA CTGTGGGCTC TATTACAGCT 4320

CAGGCTGGTG GTTTGATTCA TGTCTCTCTG CCAATTTAAA TGGCAAATAT TACCACCAGA 4380  
 AATACAAAGG TGTCCGTAAT GGGATTTTCT GGGGCACCTG GCCTGGTATA AACCAGGCAC 4440  
 AGCCAGGTGG CTACAAGTCC TCCTTCAAAC AGGCCAAGAT GATGATTAGG CCCAAGAATT 4500  
 TCAAGCCATA AATTGCTAGT GTTCATCTCT CTGGGCACTC ACTATCTAAG AGGACGATGA 4560  
 ATTCCTTCAG CCCTTTACCA TATGTCTCAG TTTATATTCC TTTCCTATGG CTAAACATTT 4620  
 CCTTTAAAGC TTTACAGCTT TTAGAATAAA GCTGAAAAGA TCTAAAAAGA CTCCTATGTT 4680  
 GCTGTTATAT GAGGAATGCT TGAAAGCACT GGAAATATTG ACAATTATAC ATTATAATTG 4740  
 CAAAACCTTT CATTTTTATT AGTTGAAAAG TTTCTAATA TTTTATTAT TTTTATAATA 4800  
 AAAACTAAAT TATTCAGCAA GCTAGATTCT ATATACGCAA GTTTTATTTT CACTAGGGCT 4860  
 AAATATACAC ATTTGAGAAT ATACCAGTCC TTCCAGGTAC AACTGAAAGC CAAGAACTGT 4920  
 AGTATTATCT TTCGTCTAAG AAGAACTTAA AGCATTTTAG TTCTCAAGAA GAAGGGCAGG 4980  
 GATGGGATTG GGGGCCAGGG ACAATATGTA TAGCTAAATG TATTCATCTA ATGCAAAATA 5040  
 TGGCATTAAA ATACCTAAAA ATGTGGTAGC ATAATATATG TCTCTTCCCT CTCCAATTGA 5100  
 AAAATAATGT TACCCTGTAG ACTTTGGTTT AGTGGTAATT CACTTACTGT TTATAGCCTG 5160  
 TTAGACCGCG ATACAAAAGC TGCTTTATCC TCTCCCTCTG CTCTCTGTGC ACAATGGTTT 5220  
 GTGATGTAAG GTGCTAGACT ACTGTAAGGT TTCCTTGGGG AAAGGCATGG TAAGGGAAAA 5280  
 CACACTGGTT TATATTTTGA AAGCCAATCC TAATCCCAA GCAATACTGT TGTCGAGGAG 5340  
 TCAACGTTCT AGGAAGCTGA CTTTCTAGA ACAAATGTAT TTATTAGGAT GAATTTGGGA 5400  
 ATT 5403

(2) INFORMATION FOR SEQ ID NO:4:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 432 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met Arg Leu Pro Gly Trp Leu Trp Leu Ser Ser Ala Val Leu Ala Ala  
 1 5 10 15  
 Cys Arg Ala Val Glu Glu His Asn Leu Thr Glu Gly Leu Glu Asp Ala  
 20 25 30  
 Ser Ala Gln Ala Ala Cys Pro Ala Arg Leu Glu Gly Ser Gly Arg Cys  
 35 40 45  
 Glu Gly Ser Gln Cys Pro Phe Gln Leu Thr Leu Pro Thr Leu Thr Ile  
 50 55 60  
 Gln Leu Pro Arg Gln Leu Gly Ser Met Glu Glu Val Leu Lys Glu Val  
 65 70 75 80



Arg Thr Leu Lys Glu Ala Val Asp Ser Leu Lys Lys Ser Cys Gln Asp  
85 90 95

Cys Lys Leu Gln Ala Asp Asp His Arg Asp Pro Gly Gly Asn Gly Gly  
100 105 110

Asn Gly Ala Glu Thr Ala Glu Asp Ser Arg Val Gln Glu Leu Glu Ser  
115 120 125

Gln Val Asn Lys Leu Ser Ser Glu Leu Lys Asn Ala Lys Asp Gln Ile  
130 135 140

Gln Gly Leu Gln Gly Arg Leu Glu Thr Leu His Leu Val Asn Met Asn  
145 150 155 160

Asn Ile Glu Asn Tyr Val Asp Asn Lys Val Ala Asn Leu Thr Val Val  
165 170 175

Val Asn Ser Leu Asp Gly Lys Cys Ser Lys Cys Pro Ser Gln Glu His  
180 185 190

Met Gln Ser Gln Pro Val Gln His Leu Ile Tyr Lys Asp Cys Ser Asp  
195 200 205

His Tyr Val Leu Gly Arg Arg Ser Ser Gly Ala Tyr Arg Val Thr Pro  
210 215 220

Asp His Arg Asn Ser Ser Phe Glu Val Tyr Cys Asp Met Glu Thr Met  
225 230 235 240

Gly Gly Gly Trp Thr Val Leu Gln Ala Arg Leu Asp Gly Ser Thr Asn  
245 250 255

Phe Thr Arg Glu Trp Lys Asp Tyr Lys Ala Gly Phe Gly Asn Leu Glu  
260 265 270

Arg Glu Phe Trp Leu Gly Asn Asp Lys Ile His Leu Leu Thr Lys Ser  
275 280 285

Lys Glu Met Ile Leu Arg Ile Asp Leu Glu Asp Phe Asn Gly Leu Thr  
290 295 300

Leu Tyr Ala Leu Tyr Asp Gln Phe Tyr Val Ala Asn Glu Phe Leu Lys  
305 310 315 320

Tyr Arg Leu His Ile Gly Asn Tyr Asn Gly Thr Ala Gly Asp Ala Leu  
325 330 335

Arg Phe Ser Arg His Tyr Asn His Asp Leu Arg Phe Phe Thr Thr Pro  
340 345 350

Asp Arg Asp Asn Asp Arg Tyr Pro Ser Gly Asn Cys Gly Leu Tyr Tyr  
355 360 365

Ser Ser Gly Trp Trp Phe Asp Ser Cys Leu Ser Ala Asn Leu Asn Gly  
370 375 380

Lys Tyr Tyr His Gln Lys Tyr Lys Gly Val Arg Asn Gly Ile Phe Trp  
385 390 395 400

Gly Thr Trp Pro Gly Ile Asn Gln Ala Gln Pro Gly Gly Tyr Lys Ser  
405 410 415

Ser Phe Lys Gln Ala Lys Met Met Ile Arg Pro Lys Asn Phe Lys Pro  
420 425 430